

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/590,146
Source: IFWP
Date Processed by STIC: 08/30/2006

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 08/30/2006
 PATENT APPLICATION: US/10/590,146 TIME: 09:07:50

Input Set : A:\2006-1392A - Sequence Listing.txt
 Output Set: N:\CRF4\08302006\J590146.raw

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3 <110> APPLICANT: Yamamoto, Hiroshi
4     Konishi, Noboru
6 <120> TITLE OF INVENTION: A method for decision of prostate tumor
8 <130> FILE REFERENCE: 09680
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/590,146
C--> 10 <141> CURRENT FILING DATE: 2006-08-21
10 <150> PRIOR APPLICATION NUMBER: JP 2004-47036
11 <151> PRIOR FILING DATE: 2004-02-23
13 <160> NUMBER OF SEQ ID NOS: 5
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1520
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (407)..(1267)
27 <400> SEQUENCE: 1
28 aggtcacaga ctgcggagtg gggtcaggggc tgcgagggct gcccgaagtc ctaccggggtt      60
30 tgcacgggcg cgcccggctc cgcccgcgaag tgcgccttcc tgacttactg ctgggtgcgc      120
32 ggggctgggg gtgcgagtac cacccttgaa gtctcttccg gggcgacctc cggggcctca      180
34 ttctaggcct ccttaaagag aaggatctaa attaggaaaa ggaagtgcc ttatccacga      240
36 ccaagctctt ccacctgcgg agctcgctta gtctgcacct caaccgtgcg gaaagtgact      300
38 gccctgttta ctgaggaaaa actggggctc agaaagatac catggagtag tttgaaacag      360
40 gaacaaaatc ttctgaaagc tcggagcaga agcctttttg gtcaac atg gag gaa      415
41                                     Met Glu Glu
42                                     1
44 aaa aga cgg cga gcc cga gtt cag gga gcc tgg gct gcc cct gtt aaa      463
45 Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala Pro Val Lys
46   5          10          15
48 agc cag gcc att gct cag cca gct acc act gct aag agc cat ctc cac      511
49 Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser His Leu His
50 20          25          30          35
52 cag aag cct ggc cag acc tgg aag aac aaa gag cat cat ctc tct gac      559
53 Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His Leu Ser Asp
54          40          45          50
56 aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt aga gct cct      607
57 Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg Arg Ala Pro
58          55          60          65
60 gag cca cga gtg att gac aga gag ggt gtg tat gaa atc agc ctg tca      655
61 Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile Ser Leu Ser
62          70          75          80
64 ccc aca ggt gta tct agg gtc tgt ttg tat cct ggc ttt gtt gac gtg      703

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65 Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe Val Asp Val
66      85              90              95
68 aaa gaa gct gac tgg ata ttg gaa cag ctt tgt caa gat gtt ccc tgg      751
69 Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp Val Pro Trp
70 100              105              110              115
72 aaa cag agg acc ggc atc aga gag gat ata act tat cag caa cca aga      799
73 Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln Gln Pro Arg
74              120              125              130
76 ctt aca gca tgg tat gga gaa ctt cct tac act tat tca aga atc act      847
77 Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser Arg Ile Thr
78              135              140              145
80 atg gaa cca aat cct cac tgg cac cct gtg ctg cgc aca cta aag aac      895
81 Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr Leu Lys Asn
82              150              155              160
84 cgc att gaa gag aac act ggc cac acc ttc aac tcc tta ctc tgc aat      943
85 Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu Leu Cys Asn
86              165              170              175
88 ctt tat cgc aat gag aag gac agc gtg gac tgg cac agt gat gat gaa      991
89 Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser Asp Asp Glu
90 180              185              190              195
92 ccc tca cta ggg agg tgc ccc att att gct tca cta agt ttt ggt gcc      1039
93 Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser Phe Gly Ala
94              200              205              210
96 aca cgc aca ttt gag atg aga aag aag cca cca cca gaa gag aat gga      1087
97 Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu Glu Asn Gly
98              215              220              225
100 gac tac aca tat gtg gaa aga gtg aag ata ccc ttg gat cat ggg acc      1135
101 Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp His Gly Thr
102              230              235              240
104 ttg tta atc atg gaa gga gcg aca caa gct gac tgg cag cat cga gtg      1183
105 Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln His Arg Val
106              245              250              255
108 ccc aaa gaa tac cac tct aga gaa ccg aga gtg aac ctg acc ttt cgg      1231
109 Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu Thr Phe Arg
110 260              265              270              275
112 aca gtc tat cca gac cct cga ggg gca ccc tgg tga cgtcagagct      1277
113 Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
114              280              285
116 ttgagagaga agcttcaactg aaacggagca aaccttccac tgagaagcca cttcaagagg      1337
118 ctggtgctgc tagatctcat gatgtggctg ttgggaagat ggtgggggttt gtttgccagc      1397
120 ttggagtcct attaaatgaa agccagcaac tcatgttggt aataggtcta ctgtgggaac      1457
122 agttatccct aaccacagct caaaatcgct atcatcttta ggcaaattaa aatctatgtg      1517
124 gca      1520
127 <210> SEQ ID NO: 2
128 <211> LENGTH: 286
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 2
134 Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala

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135 1          5          10          15
138 Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
139          20          25          30
142 His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
143          35          40          45
146 Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
147          50          55          60
150 Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
151 65          70          75          80
154 Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
155          85          90          95
158 Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
159          100          105          110
162 Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
163          115          120          125
166 Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
167          130          135          140
170 Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
171 145          150          155          160
174 Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
175          165          170          175
178 Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
179          180          185          190
182 Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
183          195          200          205
186 Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
187          210          215          220
190 Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
191 225          230          235          240
194 His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
195          245          250          255
198 His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
199          260          265          270
202 Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
203          275          280          285
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 861
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <400> SEQUENCE: 3
212 atggaggaaa aaagacggcg agcccgagtt cagggagcct gggctgcccc tgttaaaagc      60
214 caggccattg ctacagccagc taccactgct aagagccatc tccaccagaa gcctggccag      120
216 acctggaaga acaaagagca tcatctctct gacagagagt ttgtgttcaa agaacctcag      180
218 caggtagtac gtagagctcc tgagccacga gtgattgaca gagaggggtgt gtatgaaatc      240
220 agcctgtcac ccacaggtgt atctagggtc tgtttgtatc ctggctttgt tgacgtgaaa      300
222 gaagctgact ggatattgga acagctttgt caagatgttc cctggaaaca gaggaccggc      360
224 atcagagagg atataactta tcagcaacca agacttacag catggtatgg agaacttcct      420
226 tacatttatt caagaatcac tatggaacca aatcctcact ggcaccctgt gctgcgcaca      480
228 ctaaagaacc gcattgaaga gaacactggc cacaccttca actccttact ctgcaatctt      540

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230 tatcgcaatg agaaggacag cgtggactgg cacagtgatg atgaaccctc actagggagg 600
 232 tgccccatta ttgcttcact aagttttggt gccacacgca catttgagat gagaaagaag 660
 234 ccaccaccag aagagaatgg agactacaca tatgtggaaa gagtgaagat acccttggat 720
 236 catgggacct tgттаатсат ggaaggagcg acacaagctg actggcagca tcgagtgcc 780
 238 aaagaatacc actctagaga accgagagtg aacctgacct ttcggacagt ctatccagac 840
 240 cctcgagggg caccctggtg a 861

243 <210> SEQ ID NO: 4

244 <211> LENGTH: 21

245 <212> TYPE: DNA

246 <213> ORGANISM: Artificial

248 <220> FEATURE:

249 <223> OTHER INFORMATION: Oligonucleotide designed to act as PCR primer for detection

of

250 PCA-1 gene

252 <400> SEQUENCE: 4

253 ctgaaagctc ggagcagaag c

21

256 <210> SEQ ID NO: 5

257 <211> LENGTH: 18

258 <212> TYPE: DNA

259 <213> ORGANISM: Artificial

261 <220> FEATURE:

262 <223> OTHER INFORMATION: Oligonucleotide designed to act as PCR primer for detection

of

263 PCA-1 gene

265 <400> SEQUENCE: 5

266 ggtctactgt gggaacag

18

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/30/2006
PATENT APPLICATION: US/10/590,146 TIME: 09:07:51

Input Set : A:\2006-1392A - Sequence Listing.txt
Output Set: N:\CRF4\08302006\J590146.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/590,146

DATE: 08/30/2006

TIME: 09:07:51

Input Set : A:\2006-1392A - Sequence Listing.txt

Output Set: N:\CRF4\08302006\J590146.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date